



#6

SEQUENCE LISTING

<110> Denney, Jr., Dan W.

<120> Methods of Treating Lymphoma and Leukemia

<130> GENITOPE-06499

<140> 09/925,664

<141> 2001-08-09

<150> 09/370,453

<151> 1999-08-09

<150> 08/644,664

<151> 1996-05-01

<150> 08/761,277

<151> 1996-12-06

<160> 80

<170> PatentIn version 3.1

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 Met Pro Thr Arg Ser Pro Ser Val Val
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 att agc gat gat gaa cca ggt tat gac cta gat ttg ttt tgt ata cct 162
 Ile Ser Asp Asp Glu Pro Gly Tyr Asp Leu Asp Leu Phe Cys Ile Pro
 10 15 20 25
 aat cat tat gcc gag gat ttg gaa aaa gtg ttt att cct cat gga ctg 210
 Asn His Tyr Ala Glu Asp Leu Glu Lys Val Phe Ile Pro His Gly Leu
 30 35 40
 att atg gac agg act gaa aga ctt gct cga gat gtc atg aag gag atg 258
 Ile Met Asp Arg Thr Glu Arg Leu Ala Arg Asp Val Met Lys Glu Met
 45 50 55
 gga ggc cat cac att gtg gcc ctc tgt gtg ctc aag ggg ggc tat aag 306
 Gly Gly His His Ile Val Ala Leu Cys Val Leu Lys Gly Gly Tyr Lys
 60 65 70
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 Phe Phe Ala Asp Leu Leu Asp Tyr Ile Lys Ala Leu Asn Arg Asn Ser
 75 80 85
 gat aga tcc att cct atg act gta gat ttt atc aga ctg aag agc tac 402
 Asp Arg Ser Ile Pro Met Thr Val Asp Phe Ile Arg Leu Lys Ser Tyr
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Leu Ser Thr Leu Thr Gly Lys Asn Val Leu Ile Val Glu Asp Ile Ile	
125 130 135	
gac act ggt aaa aca atg caa act ttg ctt tcc ctg gtt aag cag tac	546
Asp Thr Gly Lys Thr Met Gln Thr Leu Leu Ser Leu Val Lys Gln Tyr	
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Ser Pro Lys Met Val Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser	
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cga agt gtt gga tac agg cca gac ttt gtt gga ttt gaa att cca gac	642
Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp	
170 175 180 185	
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Lys Phe Val Val Gly Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asn	
190 195 200	
ttg aat cac gtt tgt gtc att agt gaa act gga aaa gcc aaa tac aaa	738
Leu Asn His Val Cys Val Ile Ser Glu Thr Gly Lys Ala Lys Tyr Lys	
205 210 215	
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Glu Lys Val Phe Ile Pro His Gly Leu Ile Met Asp Arg Thr Glu Arg
35 40 45

Leu Ala Arg Asp Val Met Lys Glu Met Gly Gly His His Ile Val Ala
50 55 60

Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Phe Ala Asp Leu Leu Asp
65 70 75 80

Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
130 135 140

Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
165 170 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
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 Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg
 15 20 25

 aac gag ttc aag tac ttc caa aga atg acc aca acc tct tca gtg gaa 147
 Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Ser Ser Val Glu
 30 35 40 45

 ggt aaa cag aat ctg gtg att atg ggt agg aaa acc tgg ttc tcc att 195
 Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
 50 55 60

 cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt 243
 Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser
 65 70 75

 aga gaa ctc aaa gaa cca cca cga gga gct cat ttt ctt gcc aaa agt 291
 Arg Glu Leu Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser
 80 85 90

 ttg gat gat gcc tta aga ctt att gaa caa ccg gaa ttg gca agt aaa 339
 Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys
 95 100 105

 gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc 387
 Val Asp Met Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala
 110 115 120 125

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 Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln
 130 135 140

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 Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr
 145 150 155

 aaa ctt ctc cca gaa tac cca ggc gtc ctc tct gag gtc cag gag gaa 531
 Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu
 160 165 170

 aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac 573
 Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp
 175 180 185

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35 40 45

Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys
50 55 60

Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
65 70 75 80

Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
145 150 155 160

Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile
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ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc	96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile	
20 25 30	
atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg	144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	
ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag	192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	
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Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu	
65 70 75 80	
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa	288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu	
85 90 95	
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100 105 110	
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Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn	
115 120 125	
gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Val Val Asn Val	
130 135 140	
acg tgg ctt cga aat gga aaa cct gtc acc aca gga gtg tca gag aca	480
Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca aat aaa gga agt gga acc act tca ggt act acc cgt	672
Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg	
210 215 220	

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 20 25 30

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 35 40 45

Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
210 215 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225 230 235 240

Leu Val Thr Met Gly Leu Leu Thr
245

<210> 28

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 28

ccacttcctt tatttggtgc agattcag

28

<210> 29

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

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<220>

<221> CDS

<222> (1) .. (783)

<223>

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atg gtg tgt ctg aag ctc cct gga ggc tcc tgc atg aca gcg ctg aca	48
Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr	
1 5 10 15	
gtg aca ctg atg gtg ctg agc tcc cga ctg gct ttg gct ggg gac acc	96
Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr	
20 25 30	
cga cca cgt ttc ttg tgg cag ctt aag ttt gaa tgt cat ttc ttc aat	144
Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn	
35 40 45	
ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag	192
Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu	
50 55 60	
gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag	240
Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu	
65 70 75 80	
gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc	288
Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu	
85 90 95	
ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac	336
Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr	
100 105 110	
ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg	384
Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val	
115 120 125	
act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg	432
Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu	
130 135 140	
gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg	480
Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp	
145 150 155 160	
ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg	528
Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu	
165 170 175	
atc cag aat gga gat tgg acc ttc cag acc ctg gtg atg ctg gaa ata	576
Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile	
180 185 190	
gtt cct cgg agt gga gag gtt tac acc tgc caa gtg gag cac cca agt	624
Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser	
195 200 205	
gtg acg agc cct ctc aca gtg gaa tgg aga gca cgg tct gaa tct gca	672
Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala	
210 215 220	

cca aat aaa gga agt gga acc act tca ggt act acc cgt ctt cta tct	720
Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser	
225 230 235 240	

ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc	768
Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr	
245 250 255	

atg ggc ttg ctg act tag	786
Met Gly Leu Leu Thr	
260	

<210> 30

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 30

Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
1 5 10 15

Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
20 25 30

Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
35 40 45

Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
50 55 60

Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
65 70 75 80

Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
85 90 95

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
245 250 255

Met Gly Leu Leu Thr
260

<210> 31

<211> 189

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1) .. (186)

<223>

<400> 31

ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa
Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
1 5 10 15

48

cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg
Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
20 25 30

96

act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag 144
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45

gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa 189
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

<210> 32

<211> 62

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 32

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15

Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
 20 25 30

Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45

Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

<210> 33

<211> 192

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> CDS

<222> (1) .. (189)

<223>

<400> 33
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15

cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
 20 25 30

gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
 35 40 45

aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
 50 55 60

<210> 34

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 34

Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15

Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
 20 25 30

Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
 35 40 45

Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
 50 55 60

<210> 35

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 35
 cgatcgtgga tccaagtta gggtcgtatc tgtttcaaa

39

<210> 36
 <211> 34
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 36
 cgatcgagga tccaagatgg tggcagacag gacc 34
 <210> 37
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 37
 acgcgtccac catggccata agtggagtcc ct 32
 <210> 38
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 38
 ggatccaact ctgtagtctc tgggagag 28
 <210> 39
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 39
 acgcgtccac catggtgtgt ctgaagctcc tg 32

<210> 40
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 40
 ggatccaact tgctctgtgc agattcaga 29
 <210> 41
 <211> 292
 <212> DNA
 <213> Homo sapiens
 <400> 41
 gaattctttt ttgcgtgtgg cagttttaag ttattagttt ttaaaatcag tacttttttaa 60
 tggaaacaac ttgacaaaa atttgtcaca gaattttgag acccattaaa aaagttaa 120
 gagaaacctg tgtgttcctt tgggtcaacac cgagacattt aggtgaaaga catctaattc 180
 tgggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240
 gagaataggg ttgttttccc cccacataat tggaagggga aggaatatcg at 292
 <210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 42
 tcgatggcgc gccttaatta 20
 <210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

<400> 43
 agcttaatta aggcgcgcca 20

 <210> 44
 <211> 1147
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic

 <400> 44
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 agcggcggca ccgccgccct gggctgacct gtgaaggact acttccccga gcccgtagacc 120
 gtgagctgga acagcggcgc cctgaccagc ggcgtccaca cttccccgc cgtgctgcag 180
 tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240
 cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300
 gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360
 agctgcgaca cccctcccc ctgccccgc tgccccgagc ccaagagctg cgacaccct 420
 cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctcccc ctgccccgc 480
 tgccccgccc ccgagctgct gggcggcccc agcgtgttcc tgttcccccc caagcccaag 540
 gacaccctga tgatctcccg ccccccgag gtgacctgcg tgggtggtgga cgtgagccac 600
 gaggacccc aggtgcagtt caagtggtag gtggacggcg tggaggtgca taacgccaa 660
 accaagcccc gcgaggagca gtacaacagc accttccgcg tggtagagct gctgaccgtg 720
 ctgcaccagg actggctgaa cggcaaggag tacaagtga aggtgagcaa caaggccctg 780
 cccgccccca tcgagaagac catctccaag accaagggcc agccccgca gcccagggtg 840
 tacaccctgc cccccagccg cgaggagatg accaagaacc aggtgagcct gacctgcctg 900
 gtgaagggct tctaccccag cgacatcgcc gtggagtggg agagcagcgg ccagcccag 960
 aacaactaca acaccacccc cccatgctg gacagcgacg gcagcttctt cctgtacagc 1020
 aagctgaccg tggacaagag ccgctggcag cagggcaaca tcttctcctg cagcgtgatg 1080
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 tagatct 1147

<210> 45

<211> 377

<212> PRT

<213> Homo sapiens

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 46

<211> 999

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 46

gcggccgcgc gtcgaccaag ggccccagcg tggtccccct ggccccctgc agccgcagca 60
ccagcgagag caccgccgcc ctgggctgcc tggatgaagga ctacttcccc gagcccgatga 120
ccgtgagctg gaacagcggc gccctgacca gcggcgtgca caccttcccc gccgtgctgc 180

agagcagcgg cctgtactcc ctgagcagcg tggtgaccgt gcccagcagc agcctgggca 240
 ccaagaccta cacctgcaac gtggaccaca agcccagcaa caccaaggtg gacaagcgcg 300
 tggagagcaa gtacggcccc ccctgccccca gctgccccgc ccccgagttc ctgggcggcc 360
 ccagcgtggt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420
 aggtgacctg cgtgggtggtg gacgtgagcc aggaggaccc cgaggtgcag ttcaactggt 480
 acgtggacgg cgtggaggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540
 gcacctaccg cgtggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600
 agtacaagtg caaggtgtcc aacaagggcc tgcccagcag catcgagaag accatcagca 660
 aggccaaggg ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720
 tgaccaagaa ccaggtgagc ctgacctgcc tggngaaggg cttctacccc agcgacatcg 780
 ccgtggagtg ggagagcaac ggccagcccg agaacaacta caagaccacc cccccgtgc 840
 tggacagcga cggcagcttc ttctgtaca gccgcctgac cgtggacaag agccgctggc 900
 aggagggcaa cgtgttctcc tgctccgtga tgcattaggc cctgcacaac cactacaccc 960
 agaagagcct gagcctgagc ctgggcaagt gatagatct 999

<210> 47

<211> 327

<212> PRT

<213> Homo sapiens

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 48

<211> 337

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 48

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agtcggaac cgccagcgtg gtgtgcctgc tgaacaactt ctacccccgc gaggccaagg 120
tgcaagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc 180
aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact 240
acgagaagca caaggtgtac gcctgcgagg tgacccatca gggcctgagc agccccgtga 300
ccaagagctt caaccggggc gagtgctagt gagatct 337

<210> 49

<211> 106

<212> PRT

<213> Homo sapiens

<400> 49

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

134
-291

<210> 50
 <211> 346
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 50
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 gcagcgagga gctgcaggcc aacaaggcca ccctggtgtg cctgatcagc gacttctacc 120
 ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcgtggaga 180
 ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga 240
 ccccgagca gtggaagagc caccgcagct acagctgcca ggtcaccac gagggcagca 300
 ccgtggagaa gaccgtggcc cccaccgagt gcagctagtg agatct 346

<210> 51
 <211> 109
 <212> PRT
 <213> Homo sapiens
 <400> 51
 Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
 1 5 10 15
 Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
 20 25 30
 Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
 35 40 45
 Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
 50 55 60
 Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
 65 70 75 80
 Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
 85 90 95
 Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 100 105

<210> 52
 <211> 38
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 52
 tctagaattc acgcgtccac catggactgg acctggag 38
 <210> 53
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 53
 tctagaattc acgcgtccac catggacaca ctttgctaca c 41
 <210> 54
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 54
 tctagaattc acgcgtccac catggagttt gggctgagct gg 42
 <210> 55
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 55
 tctagaattc acgcgtccac catgaaacac ctgtggttct tcct 44

<210> 56
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 56
 tctagaattc acgcgtccac catggggtca accgccatcc t 41
 <210> 57
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 57
 tctagaattc acgcgtccac catgtctgtc tccttcctca tctt 44
 <210> 58
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 58
 gcctgagttc cacgacaccg tcac 24
 <210> 59
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 59
 ggggaaaagg gttggggcgg atgc 24

<210> 60
 <211> 39
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 60
 gagggggccct tggtcgacgc tgaggagacg gtgaccagg 39
 <210> 61
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 61
 gagggggccct tggtcgacgc tgaagagacg gtgaccattg 40
 <210> 62
 <211> 39
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic
 <400> 62
 gagggggccct tggtcgacgc tgaggagacg gtgaccgtg 39
 <210> 63
 <211> 45
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 63
 tctagaattc acgcgtccac catggacatg aggggtccccg ctcag 45

<210> 64
 <211> 40
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 64
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 <210> 65
 <211> 42
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 65
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 <210> 66
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic
 <400> 66
 tctagaattc acgcgtccac catggtgttg cagacccagg t 41
 <210> 67
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17